## NH C 8 JULY FE

SEQUENCE LISTING Duke University York, John D <120> NOVEL TARGETS FOR LITHIUM THERAPY AND TOXICITY TREATMENT <130> 180/158/2 <150> US 60/401480 <151> 2002-08-06 <160> 24 <170> PatentIn version 3.2 <210> <211> 2113 <212> DNA <213> Homo sapiens <220> <221> mRNA <222> (1)..(2113) <400> 1 ggaattcggc acgagaagct cggtactgga cacaacgagg gacctgggtc tacgataacg egettttget eeteetgaag tgtetttggt eeaaegttgt teeagagtgt accatggett ccagtaacac tgtgttgatg cggttggtag cctccgcata ttctattgct caaaaggcag gaatgatagt cagacgtgtt attgctgaag gagacctggg tattgtggag aagacctgtg caacagacet geagaceaaa getgacegat tggeacagat gageatatgt tetteattgg eceggaaatt eeceaaaete acaattatag gggaagagga tetgeettet gaggaagtgg atcaagaget gattgaagae agteagtggg aagaaataet gaageaacea tgeecatege agtacagtgc tattaaagaa gaagatctcg tggtctgggt tgatcctctg gatggaacca aggaatatac cgaaggtett ettgacaatg taacagttet tattggaatt gettatgaag gaaaagccat agcaggagtt attaaccagc catattacaa ctatgaggca ggaccagatg ctgtgttggg gaggacaatc tggggagttt taggtttagg cgcctttggg tttcagctga aagaagtccc tgctgggaaa cacattatca caactactcg atcccatagc aacaagttgg ttactgactg tgttgctgct atgaaccccg atgctgtgct gcgagtagga ggagcaggaa ataagattat teagetgatt gaaggeaaag eetetgetta tgtatttgea agteetggtt gtaagaagtg ggatacttgt gctccagaag ttattttaca tgctgtggga ggcaagttaa ccgatatcca tgggaatgtt cttcagtacc acaaggatgt gaagcatatg aactctgcag

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60

180

240

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720

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900

960

1020

1080

1140

1200

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Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr 35 40 45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg 50 60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu 65 70 75 80

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu 85 90 95

Lys Gln Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu 100 105 110

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly 115 120 125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys 130 140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly 145 150 155 160

Pro Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly 165 170 175

Ala Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile 180 185 190

Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala 195 200 205

Ala Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys 210 215 220

Ile Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser 225 230 235 240

Pro Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His
245 250 255

Ala Val Gly Gly Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr 260 265 270

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                                    10
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly
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100
                   105
120
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135

145 150 155 170 195 200 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa Xaa 210 215 220 Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa 230 235 250 260 265 280 Xaa Xaa 290 <210> 5 <211> 399 <212> PRT <213> Artificial <220> <223> Li-sensitive sequence uniting motif for 1ptase. <220> <221> MISC\_FEATURE <222> (1)..(53) <223> X is any amino acid. <220> <221> MISC\_FEATURE <222> (55)..(78) <223> X is any amino acid.

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Xaa	Xaa Xaa 255											
Xaa	Xaa Xaa											
Xaa	Xaa Xaa											
Xaa	Xaa Xaa											
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa 305 310 315	Xaa Xaa 320											
Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa 325 330	Xaa Xaa 335											
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Xaa 145	Xaa	Xaa	Xaa	Xaa	Xaa 150	Xaa	Xaa	Xaa	Xaa	Xaa 155	Xaa	Xaa	Xaa	Xaa	Хаа 160

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Xaa	Xaa																
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	L> ! 2> I																
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according the first according to the first ac
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taacccatgc gtatgtaatc t 981
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